

10/510, 246
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(FILE 'HOME' ENTERED AT 08:43:46 ON 23 JUL 2007)

FILE 'BIOSIS, CAPLUS, EMBASE, MEDLINE, JAPIO' ENTERED AT 08:44:04 ON 23
JUL 2007

L1	34282 S MALDI
L2	25195 S L1 AND MATRIX?
L3	97 S L2 AND EMBED?
L4	88 S L3 AND DESOR?
L5	38 S L4 AND PD<2003
L6	24 DUPLICATE REMOVE L5 (14 DUPLICATES REMOVED)
L7	3 S L6 AND CLEAV?
L8	21 S L6 NOT L7

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L7	3 S L6 AND CLEAV?
L8	21 S L6 NOT L7

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ANSWER 16 OF 21 CAPLUS COPYRIGHT 2007 ACS on STN

AN 1996:308044 CAPLUS

DN 124:335776

ED Entered STN: 25 May 1996

TI Matrix-assisted laser desorption-ionization (MALDI) mass spectrometry of biological molecules

AU Karas, M.; Bahr, U.

CS Institute Medical Physics and Biophysics, University Munster, Muenster, 48149, Germany

SO NATO ASI Series; Series C: Mathematical and Physical Sciences (1996), 475 (Mass Spectrometry in Biomolecular Sciences), 33-49
CODEN: NSCSDW; ISSN: 0258-2023

PB Kluwer

DT Journal; General Review

LA English

CC 6-0 (General Biochemistry)

Section cross-reference(s): 9

AB A review with 72 refs. Matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS) is an anal. technique for fast and precise mass determination of biol. mols. Intact mol. ions are produced by short pulsed laser irradiation of the biomols. which are embedded in a matrix consisting of small highly absorbing organic mols. Mass anal. is carried out in a linear or reflector time-of-flight mass spectrometer. The accessible mass range is 500 000 Da, a mass accuracy of up to 0.01 % can be reached, the sample amts. required are 1 pmol or less. Proteins, glycoproteins, oligonucleotides and oligosaccharides can be analyzed.

ST MALDI protein glycoproteins oligonucleotides oligosaccharides
review; mass spectrometry MALDI matrix biomol review

IT Glycoproteins, properties

Oligosaccharides

Proteins, properties

RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)

(a review of matrix-assisted laser desorption

-ionization (MALDI) mass spectrometry of biol. mols.)

IT Molecules

(biochem., a review of matrix-assisted laser desorption-ionization (MALDI) mass spectrometry of biol. mols.)

IT Nucleotides, properties

RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)

(oligo-, a review of matrix-assisted laser desorption

-ionization (MALDI) mass spectrometry of biol. mols.)

IT Mass spectrometry

(photodesorption/photoionization, laser-induced, matrix assisted; a review of matrix-assisted laser desorption-ionization (MALDI) mass spectrometry of biol. mols.)

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 ST MALDI protein glycoproteins oligonucleotides oligosaccharides review; mass spectrometry MALDI matrix biomol review
 IT Glycoproteins, properties
 Oligosaccharides
 Proteins, properties
 RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
 (a review of matrix-assisted laser desorption-ionization (MALDI) mass spectrometry of biol. mols.)
 IT Molecules
 (biochem., a review of matrix-assisted laser desorption-ionization (MALDI) mass spectrometry of biol. mols.)
 IT Nucleotides, properties
 RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
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 IT Mass spectrometry
 (photodesorption/photoionization, laser-induced, matrix assisted; a review of matrix-assisted laser desorption-ionization (MALDI) mass spectrometry of biol. mols.)

ANSWER 17 OF 21 CAPLUS COPYRIGHT 2007 ACS on STN

AN 1996:222109 CAPLUS

ED Entered STN: 16 Apr 1996

TI Functionality analysis of polymers by MALDI-MS

AU Pasch, H.

CS Deutsches Kunststoff-Institut, Darmstadt, 64289, Germany

SO Book of Abstracts, 211th ACS National Meeting, New Orleans, LA, March 24-28 (1996), POLY-374 Publisher: American Chemical Society, Washington, D. C.

CODEN: 62PIAJ

DT Conference; Meeting Abstract

LA English

AB Matrix-assisted laser desorption ionization mass

spectrometry (MALDI-MS) is a new, most promising method for the anal. of oligomers and polymers with respect to molar mass and chemical composition. By embedding macromols. in a suitable matrix and irradiating the sample with laser pulses, intact mol. ions are produced, which are analyzed in a time-of-flight mass spectrometer. A major advantage of MALDI-MS over other MS techniques is the significant reduction of fragmentation and the extended mass range. The talk will discuss the application of MALDI-MS in functionality anal. of telechelic oligomers and macromonomers. It will demonstrate that in addition to molar mass information the functionality type distribution can be obtained. In combination with liquid chromatog. MALDI-MS can be used as a molar mass and chemical composition sensitive detector.

ANSWER 19 OF 21 CAPLUS COPYRIGHT 2007 ACS on STN

AN 1994:625574 CAPLUS

DN 121:225574

ED Entered STN: 12 Nov 1994

TI Detection limits for matrix-assisted laser desorption
of polypeptides with an external ion source Fourier-transform mass
spectrometer

AU Li, Yunzhi; McIver, Robert T., Jr.

CS Dep. Chem., Univ. California, Irvine, CA, 92717, USA

SO Rapid Communications in Mass Spectrometry (1994), 8(9), 743-9
CODEN: RCMSEF; ISSN: 0951-4198

DT Journal

LA English

CC 9-5 (Biochemical Methods)

AB Sensitivity in the low-femtomole range with mass resolution greater than
20000 is demonstrated for several polypeptides analyzed by a mass
spectrometer that pairs matrix-assisted laser desorption
/ionization (MALDI) and Fourier-transform mass spectrometry
(FTMS). The compds. investigated were substance P, renin substrate,
melittin, the B-chain of the bovine insulin, and bovine insulin. Standard
solns. of the polypeptides were prepared with 30% acetonitrile + water, and
micropipettes were used to transfer small amts. (1-20 fmol) to a sample
probe. The samples were embedded in a large excess of
matrix material (2,5-dihydroxybenzoic acid) and ionized by a pulse
from an excimer laser. The FTMS instrument used for these expts. has the
MALDI source in a sep. chamber outside the magnetic field. Ions
are extracted from the source and transported by an RF-only quadrupole ion
guide to an FTMS analyzer cell mounted in the homogeneous region of a 6.5
T supercond. magnet. The high sensitivity of MALDI-FTMS is due,
in part, to the high transfer efficiency of the ion guide, even for ions
with a wide range of kinetic energies. The ion guide is easy to use
because there are only two adjustments (RF amplitude and DC offset
voltage), and unlike electrostatic ion transport means, alignment of it
with the axis of the magnetic field is not critical. The mass resolution and
sensitivity of MALDI-FTMS is compared with that of MALDI
done with time-of-flight, magnetic sector, and quadrupole ion-trap mass
spectrometers.

ST protein detection laser desorption mass spectrometry; Fourier
transform mass spectrometer protein detection

IT Ion sources
Spectrometers

(detection limits for matrix-assisted laser
desorption of polypeptides with an external ion source
Fourier-transform mass spectrometer)

IT Proteins, analysis

RL: ANT (Analyte); ANST (Analytical study)

(detection limits for matrix-assisted laser
desorption of polypeptides with an external ion source
Fourier-transform mass spectrometer)

IT 9004-10-8, Insulin, analysis

RL: ANT (Analyte); ANST (Analytical study)

(B-chain; detection limits for matrix-assisted laser
desorption of polypeptides with an external ion source
Fourier-transform mass spectrometer)

IT 11002-13-4, Renin substrate 20449-79-0, Melittin 33507-63-0, Substance
P

RL: ANT (Analyte); ANST (Analytical study)

(detection limits for matrix-assisted laser
desorption of polypeptides with an external ion source
Fourier-transform mass spectrometer)

ANSWER 19 OF 21 CAPLUS COPYRIGHT 2007 ACS on STN

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matrix material (2,5-dihydroxybenzoic acid) and ionized by a pulse
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guide to an FTMS analyzer cell mounted in the homogeneous region of a 6.5
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in part, to the high transfer efficiency of the ion guide, even for ions
with a wide range of kinetic energies. The ion guide is easy to use
because there are only two adjustments (RF amplitude and DC offset
voltage), and unlike electrostatic ion transport means, alignment of it
with the axis of the magnetic field is not critical. The mass resolution and
sensitivity of MALDI-FTMS is compared with that of MALDI
done with time-of-flight, magnetic sector, and quadrupole ion-trap mass
spectrometers:

ST protein detection laser desorption mass spectrometry; Fourier
transform mass spectrometer protein detection

IT Ion sources

Spectrometers

(detection limits for matrix-assisted laser
desorption of polypeptides with an external ion source
Fourier-transform mass spectrometer)

IT Proteins, analysis

RL: ANT (Analyte); ANST (Analytical study)

(detection limits for matrix-assisted laser
desorption of polypeptides with an external ion source
Fourier-transform mass spectrometer)

IT 9004-10-8, Insulin, analysis

RL: ANT (Analyte); ANST (Analytical study)

(B-chain; detection limits for matrix-assisted laser
desorption of polypeptides with an external ion source
Fourier-transform mass spectrometer)

IT 11002-13-4, Renin substrate 20449-79-0, Melittin 33507-63-0, Substance
P

RL: ANT (Analyte); ANST (Analytical study)

(detection limits for matrix-assisted laser
desorption of polypeptides with an external ion source
Fourier-transform mass spectrometer)

AN 2001:609580 CAPLUS
DN 136:263433
ED Entered STN: 22 Aug 2001
TI N-C α bond cleavage of the peptide backbone via hydrogen abstraction
AU Takayam, Mitsuo
CS Graduate School of Sciences, Yokohama City University, Yokohama, 236-0027, Japan
SO Journal of the American Society for Mass Spectrometry (2001), 12(9), 1044-1049
CODEN: JAMSEF; ISSN: 1044-0305
PB Elsevier Science Inc.
DT Journal
LA English
CC 34-3 (Amino Acids, Peptides, and Proteins)
Section cross-reference(s): 22, 73
AB The specific cleavage of N-C α bonds on the peptide backbone to form the so-called 'c' and 'z +2' products, which can be used for the rapid determination of protein amino-acid sequences, has been examined to clarify the mechanism(s) that occur during hydrogen abstraction induced by bombardment with 337-nm laser photons in matrix-assisted laser desorption/ionization (MALDI) method. Intramol. hydrogen abstraction, which results from the hydrogen(s) on the C α or C β carbon, did not occur with a deuterium-labeled dodecapeptide. To confirm a proposition that intermol. hydrogen abstraction occurs between the peptide and the MALDI matrix, a deuterium dodecapeptide embedded in a deuterium 2,5-dihydroxybenzoic acid matrix at a molar ratio of 1:7000 was analyzed. The resulting deuterium c product ions suggested that c ions form via intermol. hydrogen abstraction, although the results obtained did not deny any other possibilities such as intramol. transfer of labile hydrogen. A mechanism for the N-C α bond cleavage has been proposed that the formation of hypervalent radical species and subsequent prompt bond cleavages occur. The proposed mechanism successfully rationalizes the formation of both the z +2 and the c product ions.

ST bond cleavage peptide MALDI deuterium exchange mol structure detn
IT Laser ionization mass spectrometry
(photodesorption, matrix-assisted; study of N-C α bond cleavage of the peptide backbone via hydrogen abstraction using MALDI and deuterium exchange techniques)

IT Laser desorption mass spectrometry
(photoionization, matrix-assisted; study of N-C α bond cleavage of the peptide backbone via hydrogen abstraction using MALDI and deuterium exchange techniques)

IT Bond cleavage
Exchange reaction
Molecular structure determination methods
(study of N-C α bond cleavage of the peptide backbone via hydrogen abstraction using MALDI and deuterium exchange techniques)

IT Peptides, properties
RL: PRP (Properties)
(study of N-C α bond cleavage of the peptide backbone via hydrogen abstraction using MALDI and deuterium exchange techniques)

IT 404956-26-9 404956-28-1
RL: PRP (Properties)
(study of N-C α bond cleavage of the peptide backbone via hydrogen abstraction using MALDI and deuterium exchange techniques)

RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

- (1) Barber, M; J C S Chem Commun 1981, P325 CAPLUS
- (2) Biemann, K; Biomed Environ Mass Spectrom 1988, V16, P99 MEDLINE
- (3) Brown, R; Anal Chem 1995, V67, P3990 CAPLUS
- (4) Brown, R; J Am Soc Mass Spectrom 1996, V7, P225 CAPLUS
- (5) de Heer, M; J Am Chem Soc 2000, V122, P2355 CAPLUS
- (6) Harvey, D; Org Mass Spectrom 1993, V28, P287 CAPLUS
- (7) Karas, M; Int J Mass Spectrom Ion Processes 1987, V78, P53 CAPLUS
- (8) Lennon, J; Protein Science 1997, V6, P2446 CAPLUS
- (9) Lennon, J; Protein Science 1999, V8, P2487 CAPLUS
- (10) Lockyer, N; Int J Mass Spectrom 1998, V176, P77 CAPLUS
- (11) Mahoney, J; Rapid Commun Mass Spectrom 1991, V5, P441 CAPLUS
- (12) Nagaoka, S; J Phys Chem 1992, V96, P2754 CAPLUS
- (13) Nielsen, M; Chem Phys Lett 2000, V330, P558 CAPLUS
- (14) Olumee, Z; Rapid Commun Mass Spectrom 1995, V9, P744 CAPLUS
- (15) Reiber, D; Anal Chem 1998, V70, P673 CAPLUS
- (16) Rodriguez-Santiago, L; J Phys Chem A 2000, V104, P1256 CAPLUS
- (17) Strupat, K; Int J Mass Spectrom Ion Processes 1991, V111, P89 CAPLUS
- (18) Strupat, K; Int J Mass Spectrom Ion Processes 1997, V169/170, P43 CAPLUS
- (19) Surman, D; J C S Commun 1981, P324 CAPLUS
- (20) Takayama, M; Int J Mass Spectrom 1998, V181, PL1 CAPLUS
- (21) Takayama, M; J Am Soc Mass Spectrom 2001, V12, P420 CAPLUS
- (22) Vidavsky, I; J Am Chem Soc 1994, V116, P5865 CAPLUS
- (23) Vorst, H; Rapid Commun Mass Spectrom 1990, V4, P202 CAPLUS
- (24) Williams, D; J Am Chem Soc 1981, V103, P5700 CAPLUS
- (25) Yamashita, M; J Phys Chem 1984, V88, P4451 CAPLUS
- (26) Zubarev, R; J Am Chem Soc 1998, V120, P3265 CAPLUS
- (27) Zubarev, R; J Am Chem Soc 1999, V121, P2857 CAPLUS

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CODEN: JAMSEF; ISSN: 1044-0305
PB Elsevier Science Inc.
DT Journal
LA English
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Exchange reaction
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(study of N-C α bond cleavage of the peptide backbone via hydrogen abstraction using MALDI and deuterium exchange techniques)
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- (8) Lennon, J; Protein Science 1997, V6, P2446 CAPLUS
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- (12) Nagaoka, S; J Phys Chem 1992, V96, P2754 CAPLUS
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- (14) Olumee, Z; Rapid Commun Mass Spectrom 1995, V9, P744 CAPLUS
- (15) Reiber, D; Anal Chem 1998, V70, P673 CAPLUS
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- (23) Vorst, H; Rapid Commun Mass Spectrom 1990, V4, P202 CAPLUS
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- (25) Yamashita, M; J Phys Chem 1984, V88, P4451 CAPLUS
- (26) Zubarev, R; J Am Chem Soc 1998, V120, P3265 CAPLUS
- (27) Zubarev, R; J Am Chem Soc 1999, V121, P2857 CAPLUS

AN 1994:265061 CAPLUS
DN 120:265061
ED Entered STN: 28 May 1994
TI Time-of-Flight Mass Spectrometry Of Underivatized Single-Stranded DNA
Oligomers by Matrix-Assisted Laser Desorption
AU Wu, Kuang Jen; Shaler, Thomas A.; Becker, Christopher H.
CS Molecular Physics Laboratory, SRI International, Menlo Park, CA, 94025,
USA
SO Analytical Chemistry (1994), 66(10), 1637-45
CODEN: ANCHAM; ISSN: 0003-2700
DT Journal
LA English
CC 9-5 (Biochemical Methods)
Section cross-reference(s): 6, 73
AB Matrix-assisted laser desorption with concomitant
ionization (MALDI) in conjunction with time-of-flight mass
spectrometry (TOF-MS) has been used to analyze underivatized random-base
single-stranded DNA (ssDNA) oligomers ranging from 10 to 89 nucleotides in
length by embedding them in a solid matrix of
3-hydroxypicolinic acid. At 355-nm desorption wavelength, mass
spectra of pos. and neg. ions measured by reflecting and linear
time-of-flight mass spectrometers are compared. Results from the linear
system show the ionization yield is approx. equal for each polarity.
Metastable ion decay is significant for the larger ssDNA oligomer ions,
which results in a decrease in signal intensity and the broadening of mass
peaks. To obtain an acceptable signal-to-noise ratio on a reflecting TOF
system, a higher laser irradiance is needed, which consequently causes
further degradation of mass resolution. With the apparent advantages of better
sensitivity and mass resolution, it is concluded that a linear TOF system is
better suited for the mass spectrometric anal. of ssDNA oligomers larger
than about a 25-mer. The current system permits one-base resolution up to
about a 40-mer. Mass accuracy for a 20-mer or smaller is within
 $\pm 0.05\%$. Comparison of mass spectra from 5-ns and 35-ps pulse widths at
the same energy d. shows no significant differences. Mechanisms for
oligonucleotide ion production in these expts. are discussed.
ST DNA mass spectrometry laser desorption; time of flight mass
spectrometry DNA; hydroxypicolinate matrix DNA mass spectrometry
IT Mass spectra
(of underivatized single-stranded DNA oligomers)
IT Deoxyribonucleic acids
RL: ANST (Analytical study)
(single-stranded, time-of-flight mass spectrometry of underivatized, by
matrix-assisted laser desorption)
IT Mass spectrometry
(photodesorption, laser-induced, matrix-assisted, of
underivatized single-stranded DNA oligomers)
IT Mass spectrometry
(time-of-flight, of underivatized single-stranded DNA oligomers)
IT 874-24-8, 3-Hydroxypicolinic acid
RL: ANST (Analytical study)
(in time-of-flight mass spectrometry of underivatized single-stranded
DNA oligomers)

ANSWER 20 OF 21 CAPLUS COPYRIGHT 2007 ACS on STN

AN 1994:265061 CAPLUS

DN 120:265061

ED Entered STN: 28 May 1994

TI Time-of-Flight Mass Spectrometry Of Underivatized Single-Stranded DNA Oligomers by Matrix-Assisted Laser Desorption

AU Wu, Kuang Jen; Shaler, Thomas A.; Becker, Christopher H.

CS Molecular Physics Laboratory, SRI International, Menlo Park, CA, 94025, USA

SO Analytical Chemistry (1994), 66(10), 1637-45

CODEN: ANCHAM; ISSN: 0003-2700

DT Journal

LA English

CC 9-5 (Biochemical Methods)

Section cross-reference(s): 6, 73

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ST DNA mass spectrometry laser desorption; time of flight mass spectrometry DNA; hydroxypicolinate matrix DNA mass spectrometry

IT Mass spectra
(of underivatized single-stranded DNA oligomers)

IT Deoxyribonucleic acids

RL: ANST (Analytical study)

(single-stranded, time-of-flight mass spectrometry of underivatized, by matrix-assisted laser desorption)

IT Mass spectrometry

(photodesorption, laser-induced, matrix-assisted, of underivatized single-stranded DNA oligomers)

IT Mass spectrometry

(time-of-flight, of underivatized single-stranded DNA oligomers)

IT 874-24-8, 3-Hydroxypicolinic acid

RL: ANST (Analytical study)

(in time-of-flight mass spectrometry of underivatized single-stranded DNA oligomers)

ANSWER 17 OF 21 CAPLUS COPYRIGHT 2007 ACS on STN

AN 1996:222109 CAPLUS

ED Entered STN: 16 Apr 1996

TI Functionality analysis of polymers by MALDI-MS

AU Pasch, H.

CS Deutsches Kunststoff-Institut, Darmstadt, 64289, Germany

SO Book of Abstracts, 211th ACS National Meeting, New Orleans, LA, March
24-28 (1996), POLY-374 Publisher: American Chemical Society,
Washington, D. C.

CODEN: 62PIAJ

DT Conference; Meeting Abstract

LA English

AB Matrix-assisted laser desorption ionization mass

spectrometry (MALDI-MS) is a new, most promising method for the
anal. of oligomers and polymers with respect to molar mass and chemical
composition. By embedding macromols. in a suitable matrix
and irradiating the sample with laser pulses, intact mol. ions are
produced, which are analyzed in a time-of-flight mass spectrometer. A
major advantage of MALDI-MS over other MS techniques is the
significant reduction of fragmentation and the extended mass range. The talk
will discuss the application of MALDI-MS in functionality anal.
of telechelic oligomers and macromonomers. It will demonstrate that in
addition to molar mass information the functionality type distribution can be
obtained. In combination with liquid chromatog. MALDI-MS can be
used as a molar mass and chemical composition sensitive detector.